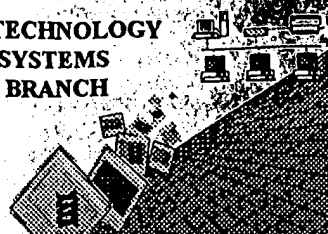


K. Davis

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BIOTECHNOLOGY  
SYSTEMS  
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Revised 01/29/2002



1600

## RAW SEQUENCE LISTING

DATE: 02/14/2002

PATENT APPLICATION: US/09/487,558A

TIME: 14:23:29

Input Set : D:\MIC-001USptn.ST25.txt

Output Set: N:\CRF3\02142002\I487558A.raw

**Does Not Comply  
Corrected Diskette Needed**

4 <110> APPLICANT: Busby, Robert  
 5 Cali, Brian  
 6 Hecht, Peter  
 7 Holtzman, Doug  
 8 Madden, Kevin  
 9 Maxon, Mary  
 10 Milne, Todd  
 11 Norman, Thea  
 12 Royer, John  
 13 Salama, Sofie  
 14 Sherman, Amir  
 15 Silva, Jeff  
 16 Summers, Eric  
 18 <120> TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in  
 Fungi  
 20 <130> FILE REFERENCE: 109272.130  
 W--> 22 ~~<130> FILE REFERENCE: 109272-130~~ *delete - already shown above*  
 24 <140> CURRENT APPLICATION NUMBER: 09/487,558A  
 25 <141> CURRENT FILING DATE: 2000-01-19  
 27 <150> PRIOR APPLICATION NUMBER: US 60/487,558  
 28 <151> PRIOR FILING DATE: 1999-10-20  
 E--> 30 <160> NUMBER OF SEQ ID NOS: 440 *446 (p. 2)*  
 32 <170> SOFTWARE: PatentIn version 3.0

ERRORED SEQUENCES

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<211> 24  
<212> DNA  
<213> *Saccaromyces cerevesiae*

<400> 446  
gttaagcagg aattaccgac acca

24

FYI Review the Sequence Listing to insure a corresponding  
explanation is presented in the <220> to <223> fields of  
each sequence using n or Xaa.

~~VERIFICATION SUMMARY~~

~~DATE: 02/14/2002~~

PATENT APPLICATION: US/09/487,558A

TIME: 14:23:38

Input Set : D:\MIC-001USptn.ST25.txt

Output Set: N:\CRF3\02142002\I487558A.raw

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L:99 M:283 W: Missing Blank Line separator, <220> field identifier  
L:112 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8  
L:113 M:283 W: Missing Blank Line separator, <220> field identifier  
L:126 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:9  
L:127 M:283 W: Missing Blank Line separator, <220> field identifier  
L:140 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10  
L:141 M:283 W: Missing Blank Line separator, <220> field identifier  
L:30 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (440) Counted (446)